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Typed or Printed Name	Susan M. Alessi		
Signature	<i>Susan M. Alessi</i>	Date	August 20, 2002
<b>INFORMATION DISCLOSURE STATEMENT</b>		Attorney Docket	AGYT-011CIP2
Address to: Commissioner for Patents Washington, D.C. 20231		First Named Inventor	MURRAY, JOSEPH
		Application Number	10/090,698
		Confirmation No.	5398
		Filing Date	March 4, 2002
		Group Art Unit	1637
		Examiner Name	
Title: "AUTOMATED PATHWAY RECOGNITION SYSTEM"			

Sir:

This is an Information Disclosure Statement submitted for the Examiner's consideration. A Form PTO-SB/08A listing the references and copies of the cited references accompany this paper. Applicants would appreciate the Examiner's initialing and returning the form to indicate that the references have been reviewed and made of record.

**Some of the references identified herein were disclosed in parent application serial number 09/365,587, filed 7/30/1999 and as such, copies thereof are not included pursuant to the provisions of 37 CFR § 1.98(d).**

This Information Disclosure Statement is not intended as a representation that a search has been made, that additional information material to the examination of this application does not exist, or that any one of the above references constitutes prior art to the present application within the meaning of 35 U.S.C. § 102.

As applicants have not yet received a first Action on the merits, no fee is believed to be required for filing this Disclosure Statement. If, however, the PTO finds that for some reason a fee is due, our Deposit Account No. 50-0815, Order No. AGYT-011CIP2 may be charged thereon.

Respectfully submitted,  
BOZICEVIC, FIELD & FRANCIS LLP

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Date: August 20, 2002

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<p>Substitute for form 1449A/PTO</p> <p><b>INFORMATION DISCLOSURE STATEMENT BY APPLICANT</b></p> <p>(use as many sheets as necessary)</p>				<b>Complete if Known</b>	
				Application Number	10/090,698
				Filing Date	March 4, 2002
				First Named Inventor	MURRAY et al.
				Group Art Unit	1637
				Examiner Name	
Sheet	1	of	3	Attorney Docket Number	AGYT-011CIP

<b>U.S. PATENT DOCUMENTS</b>					
Examiner Initials <sup>1</sup>	Cite No. <sup>1</sup>	U.S. Patent Documents		Name of Patentee or Applicant of Cited Documents	Date of Publication of Cited Document MM-DD-YYYY
		Number	Kind Code <sup>2</sup> (if known)		
		5,593,839		Hubbell, et al.	01-14-1997
		5,807,522		Brown, et al.	09-15-1998
		5,942,399		Hillman, et al.	08-24-1999
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		6,189,013		Maslyn et al.	02-2000
		6,023,659		Seilhamer, et al.	02-08-2000

<b>FOREIGN PATENT DOCUMENTS</b>					
Examiner Initials <sup>1</sup>	Cite No. <sup>1</sup>	Foreign Patent Documents		Name of Patentee or Applicant of Cited Documents	Date of Publication of Cited Document MM-DD-YYYY
		Office <sup>3</sup>	Number <sup>4</sup> Kind Code <sup>5</sup> (if known)		
		WO/9915626		Greenwald et al.	04-1999

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<b>NON PATENT LITERATURE DOCUMENTS</b>					
Examiner Initials <sup>1</sup>	Cite No. <sup>1</sup>	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc.), date, page(s), volume-issue number(s), publisher city and/or country where published			
		ANDRADE, et al. "Automatic extraction of keywords from scientific text: Application to the knowledge domain of protein families", <i>Bioinformatics</i> , (1998) Vol. 14(7): 600-60.			
		ANDRADE, et al. "Automated extraction of information in molecular biology", <i>FEBS</i> , (2000) Vol. 476: 12-17.			
		BECKER, et al. "A graph layout algorithm for drawing metabolic pathways", <i>Bioinformatics</i> , (2001) Vol. 17(5): 461-467.			
		BROWN, et al. "Knowledge-based analysis of microarray gene expression data by using support vector machines", <i>Proc. Natl. Acad. Sci. USA</i> , (2000) Vol. 97: 262-267.			
		EISEN, et al. "Cluster analysis and display of genome-wide expression patterns", <i>Proc. Natl. Acad. Sci. USA</i> , (1998) Vol. 95: 14863-14868.			
		FRIEDMAN, et al. "Genies: A natural-language processing system for the extraction of molecular pathways from journal articles", <i>Bioinformatics</i> , (2001) Vol. 17(Suppl. 1): S74-S82.			

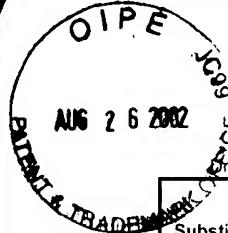
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Sheet

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of

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## Complete if Known

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		FUKUDA, et al. "Toward information extraction: Identifying protein names from biological papers", <i>Proc. of the Pacific Symposium on Biocomputing</i> (1998): 707-719.	
		FUKUDA, et al. "Knowledge representation of signal transduction", <i>Bioinformatics</i> , (2001) Vol. 17(9): 829-837.	
		HUA et al., "Construction of a modular yeast two hybrid cDNA library from human EST clones for the human genome protein linkage map, " <i>Gene</i> , 1998, vol. 215, no. 1, pp. 143-152.	
/		HISHIKI, et al. "Developing NLP tools for genome informatics: An information extraction perspective", <i>Genome Informatics</i> , (1998) Vol. 9: 81-90.	
/		HUMPHREYS, et al. "Automatically extracting enzyme interaction and protein structure information from Biological Science journal articles", <i>Proc. of the Symposium on Artificial Intelligence in Bioinformatics of the 2000 Convention of the Society for the Study of Artificial Intelligence and the Simulation of Behaviour</i> , (2000) (AISB-00), Birmingham, UK: 17-20.	
/		INGRAM et al., "Developing mouse models of aging: a consideration of strain differences in age-related behavioral and neural parameters," <i>Neurobiology of Aging</i> , 1999, vol. 20, no. 2, pp. 137-145.	
		KRAUTHAMMER, et al. "Using BLAST for identifying gene and protein names in journal articles", <i>Gene</i> , (2000) Vol. 259: 245-252.	
		MARCOTTE, et al. "Mining literature for protein-protein interactions", <i>Bioinformatics</i> , (2001) Vol. 17(4): 359-363.	
/		MASYS, et al. "Use of keyword hierarchies to interpret gene expression patterns", <i>Bioinformatics</i> , (2001) Vol. 17(4): 319-326.	
/		MROWKA. "A Java applet for visualizing protein-protein interaction", <i>Bioinformatics</i> , (2001) Vol. 17(7): 669-670.	
X		NEVILL-MANNING, Craig G., "Highly Specific Protein Sequence Motifs for Genome Analysis", <i>Colloquium Paper, Prof. Natl. Acad. Sci. USA</i> , (1998), Vol. 95, pp. 5865-5871	
/		NG, et al. "Toward routine automatic pathway discovery from on-line scientific text abstracts", <i>Genome Informatics</i> , (1999) Vol. 10: 104-112.	
		ONO, et al. "Automated extraction of information on protein-protein interactions from the biological literature", <i>Bioinformatics</i> , (2001) Vol. 17(2): 155-161.	

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✓		PROUX, et al. "Detecting gene symbols and names in biological texts: A first step toward pertinent information extraction", <i>Genome Inf.</i> , Vol. 9: 72-80 (1988).	
✓		RAYCHAUDHURI, et al. "Basic microarray analysis: Grouping and feature reduction", <i>Trends in Biotechnology</i> , (2001) Vol. 19(5): 189-193.	
✓		RAYCHAUDHURI, et al. "Associating genes with gene ontology codes using a maximum entropy analysis of biomedical literature", <i>Genome Res.</i> (2002) Vol. 12: 203-214.	
✓		RINDFLESCH, et al. "Mining molecular binding terminology from biomedical text", <i>Proc. AMIA Symposium</i> , (1999): 127-131.	
✓		SALAMONSEN, et al. "BioJAKE: A tool for the creation, visualization, and manipulation of metabolic pathways", <i>Proc. of the Pacific Symposium on Biocomputing</i> 1999, (1999).	
✓		SEKIMIZU, et al. "Identifying the interaction between genes and gene products based on frequently seen verbs in Medline abstracts", <i>Genome Inf.</i> , (1998) Vol. 9: 62-71	
✓		SCHATZ. "Information retrieval in digital libraries: Bringing search to the net", <i>Science</i> , (1997) Vol. 275(5298): 327-334.	
✓		STEPHENS, et al. "Detecting gene relationships from Medline abstracts", <i>Proc. of the Pacific Symposium on Biocomputing</i> , (2001): 483-495.	
✓		TAMAYO, et al. "Interpreting patterns of gene expression with self-organizing maps: Methods and application to hematopoietic differentiation", <i>Proc. Natl. Acad. Sci. USA</i> , (1999) Vol. 96: 2907-2912.	
✓		THOMAS, et al. "Automatic extraction of protein interactions from scientific abstracts", <i>Proc. of the Pacific Symposium on Biocomputing</i> , (2000): 538-549.	
✓		WONG. "A protein interaction extraction system", <i>Proc. of the Pacific Symposium on Biocomputing</i> 2001, (2001): 1-11.	
✓		YOSHIDA, et al. "PNAD-CSS: A workbench for constructing a protein name abbreviation dictionary", <i>Bioinformatics</i> , (2000) Vol. 16(2): 169-175.	

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